ASAP Web results

date:2023-02-14T10:21:42
input file:Stictochironomus-Alignment-3.fas.phy.reduced-5.fas
nb of sequences:218
length of seqs:658
subst. model:K80 Kimura
recurs split pval:1.000000e-02

Split probability: 0.010000 sequence length: 658

Save Spart text File **here**

Save Spart XML File **here**

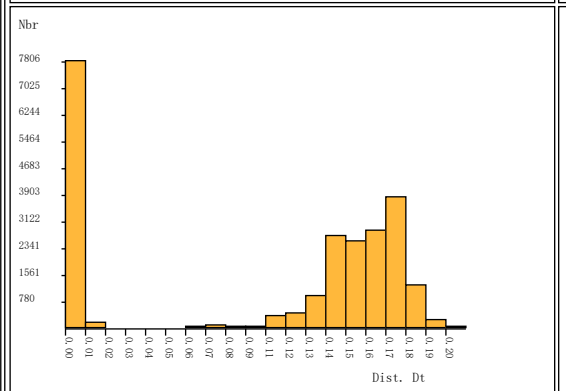
10 best partitions found by ASAP (see **FAQ** for more details)

The lower the score, the better the partition

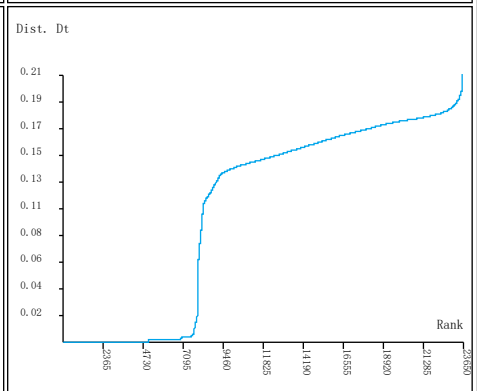
Nb of subsets	asap-score	P-val (rank)	W (rank)	Treshold dist.	Text
21	4.00	1.54e-01 (3)	1.59e-04 (5)	0.069020	**list csv**
* 24	4.50	2.16e-01 (6)	2.48e-03 (3)	0.048527	**list csv**
19	6.00	4.29e-02 (2)	1.18e-04 (10)	0.073653	**list csv**
23	6.50	2.85e-01 (9)	3.82e-04 (4)	0.056231	**list csv**
* 41	9.50	2.71e-01 (8)	1.15e-04 (11)	0.008379	**list csv**
16	11.00	3.77e-01 (14)	1.47e-04 (8)	0.088886	**list csv**
* 37	12.00	1.74e-01 (4)	7.54e-05 (20)	0.009415	**list csv**
12	17.00	1.00e-05 (1)	4.00e-05 (33)	0.104006	**list csv**
* 44	17.00	3.09e-01 (11)	7.11e-05 (23)	0.006204	**list csv**
13	19.00	3.63e-01 (13)	6.97e-05 (25)	0.101450	**list csv**

Number of subsets in this table equals to the number of primary species hypotheses in the respective partition

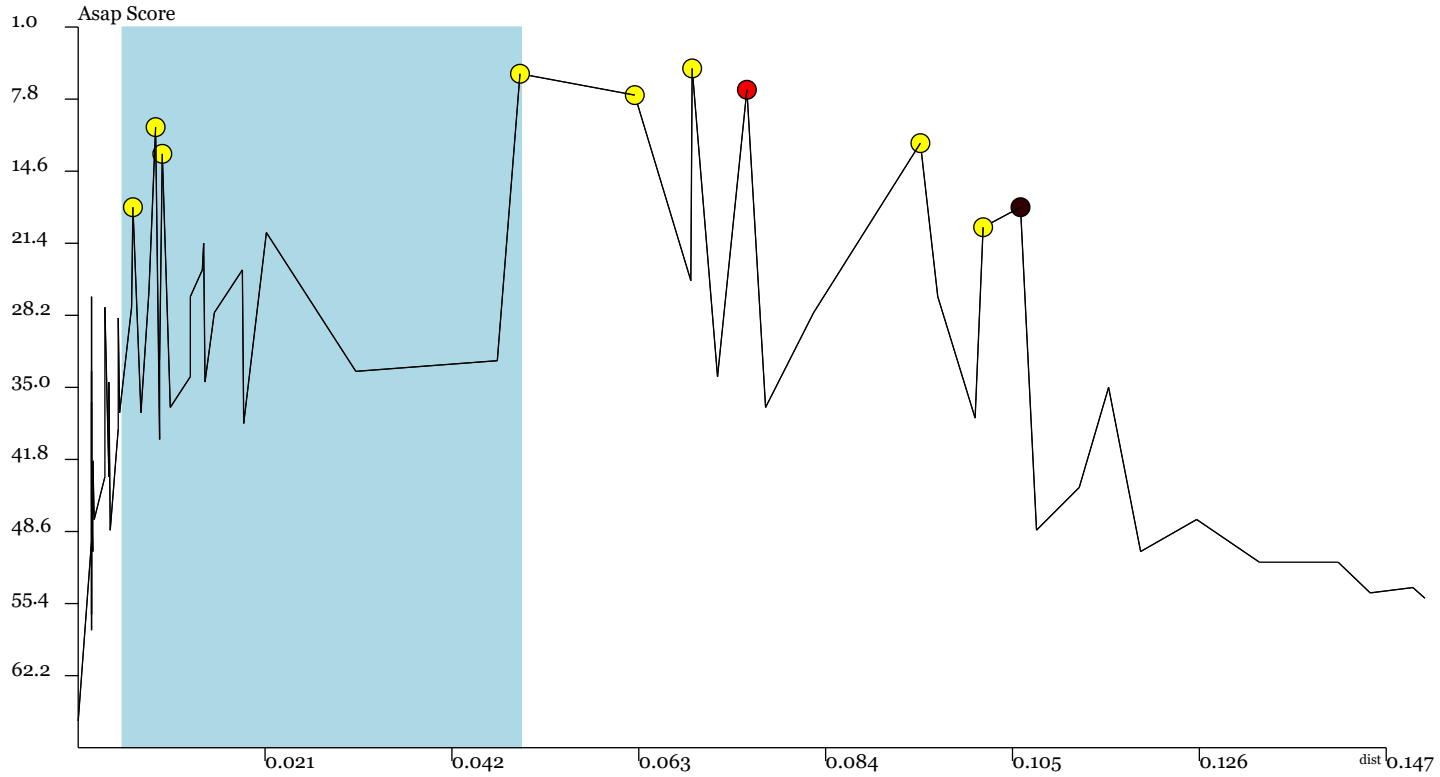
Histogram of distances **[save]**



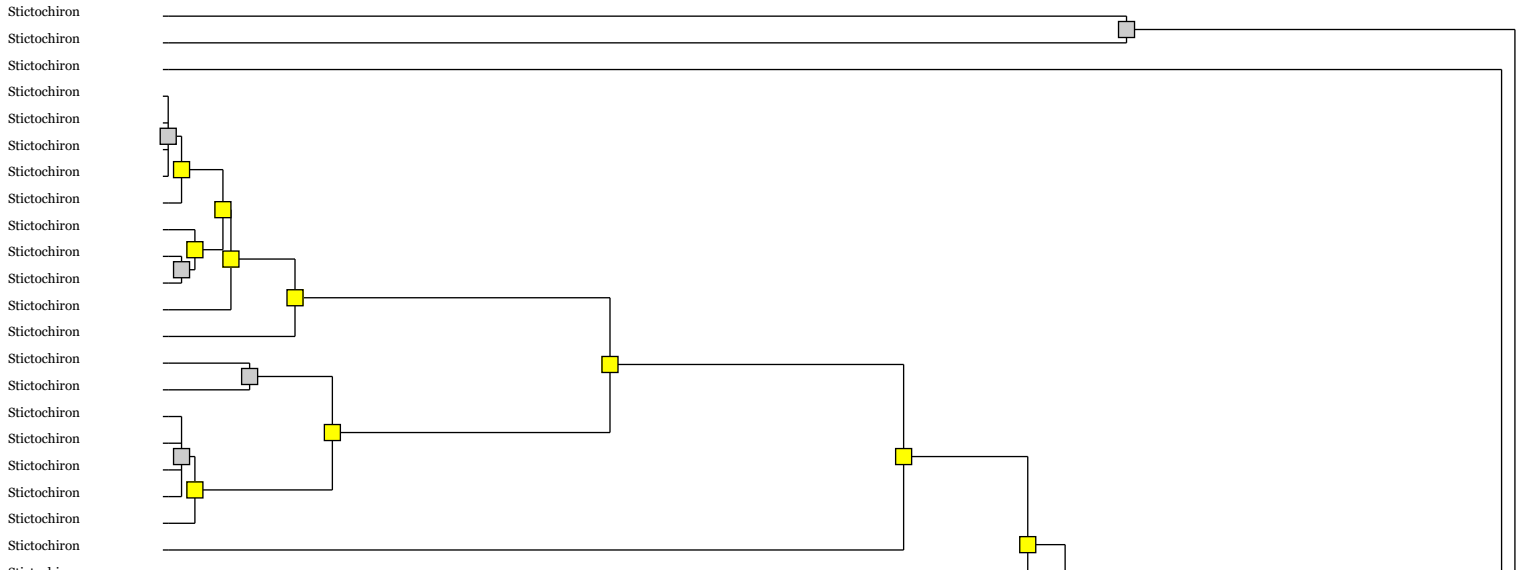
Ranked distances **[save]**



View/Save Boxed subsets graph **here**



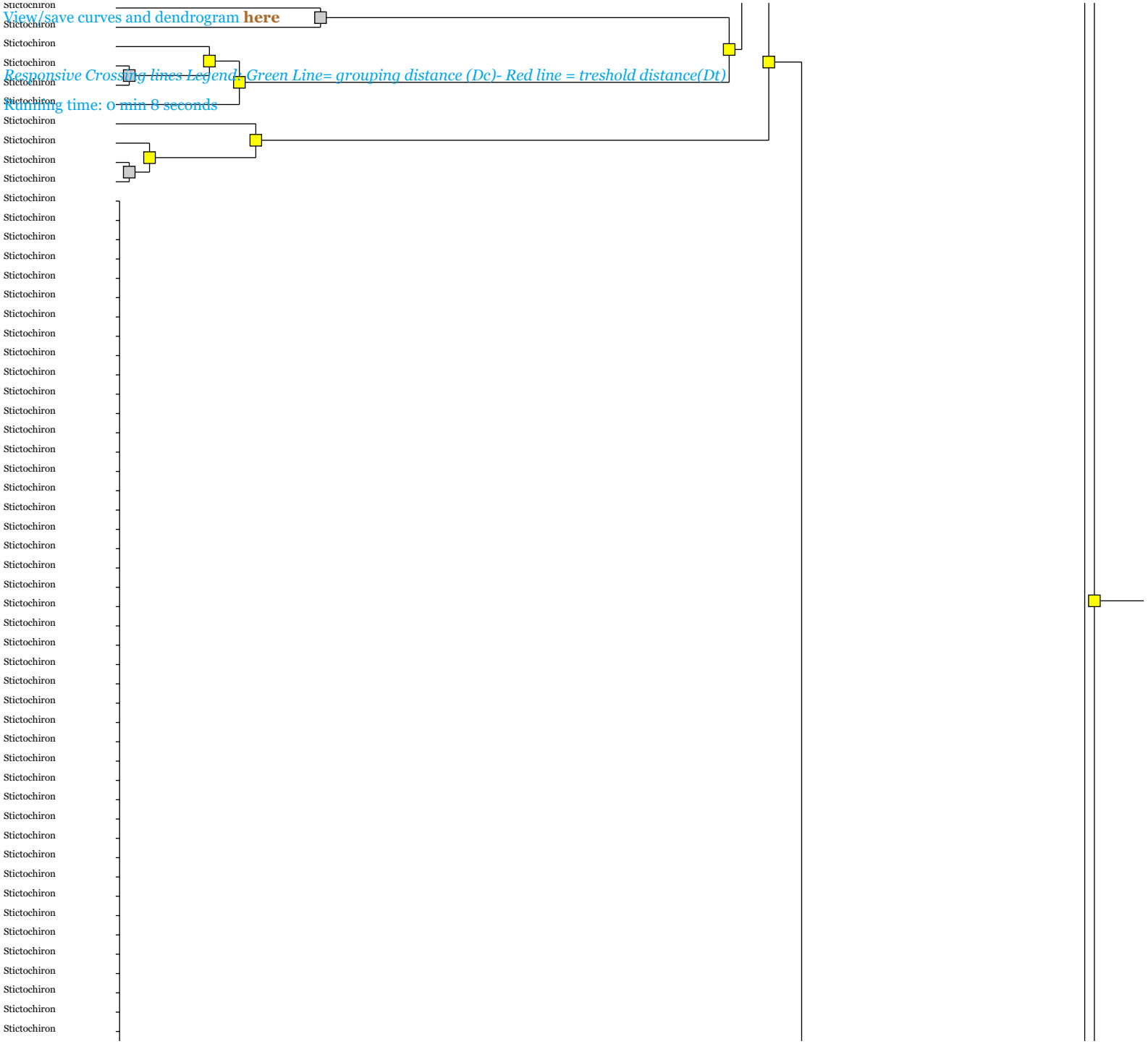
Legend: <0.001 <0.05 <0.1 >0.1 N/A

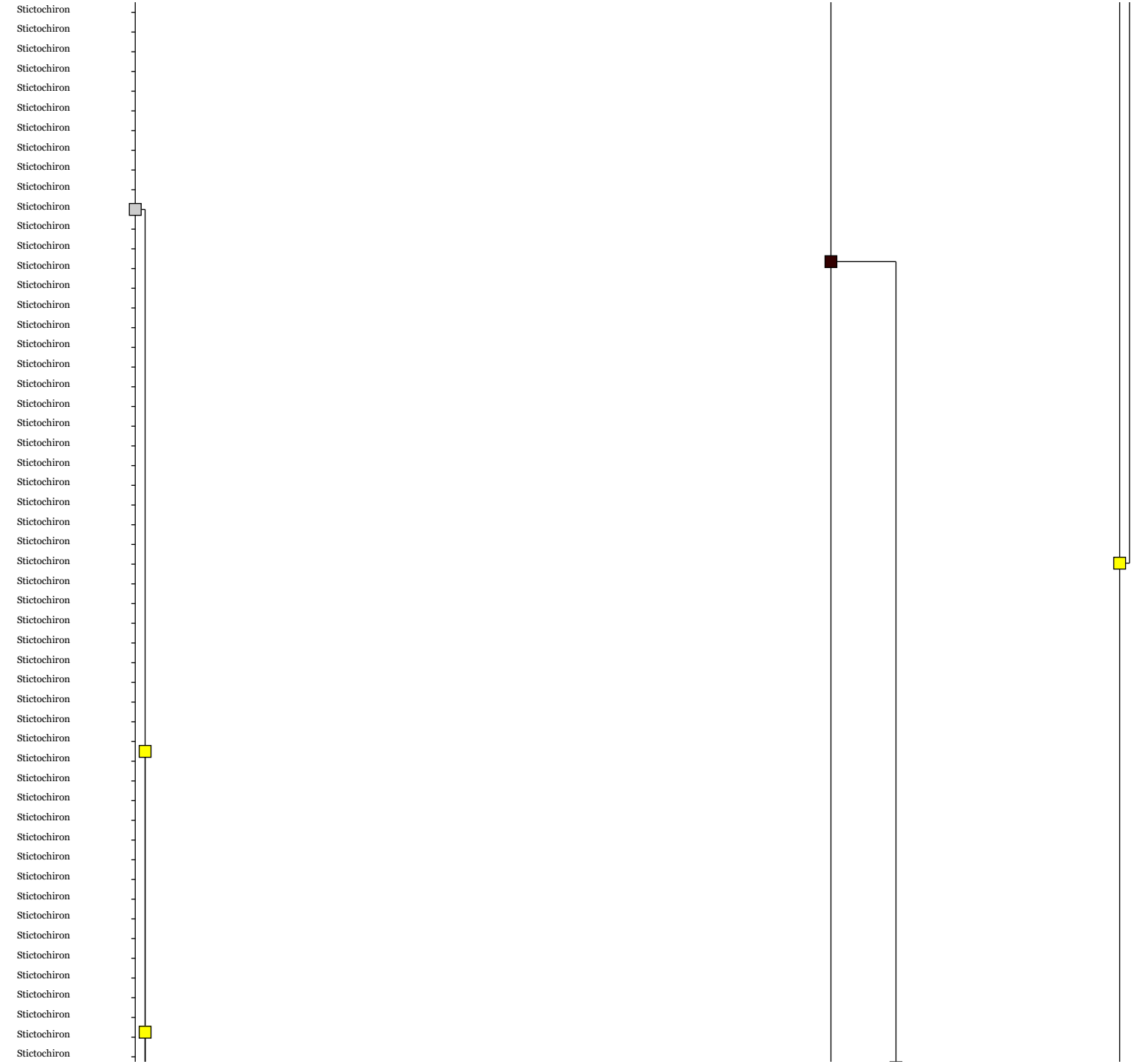


View/save curves and dendrogram **here**

Responsive Crossing lines Legend: Green Line= grouping distance (Dc)- Red line = treshold distance(Dt)

Running time: 0 min 8 seconds

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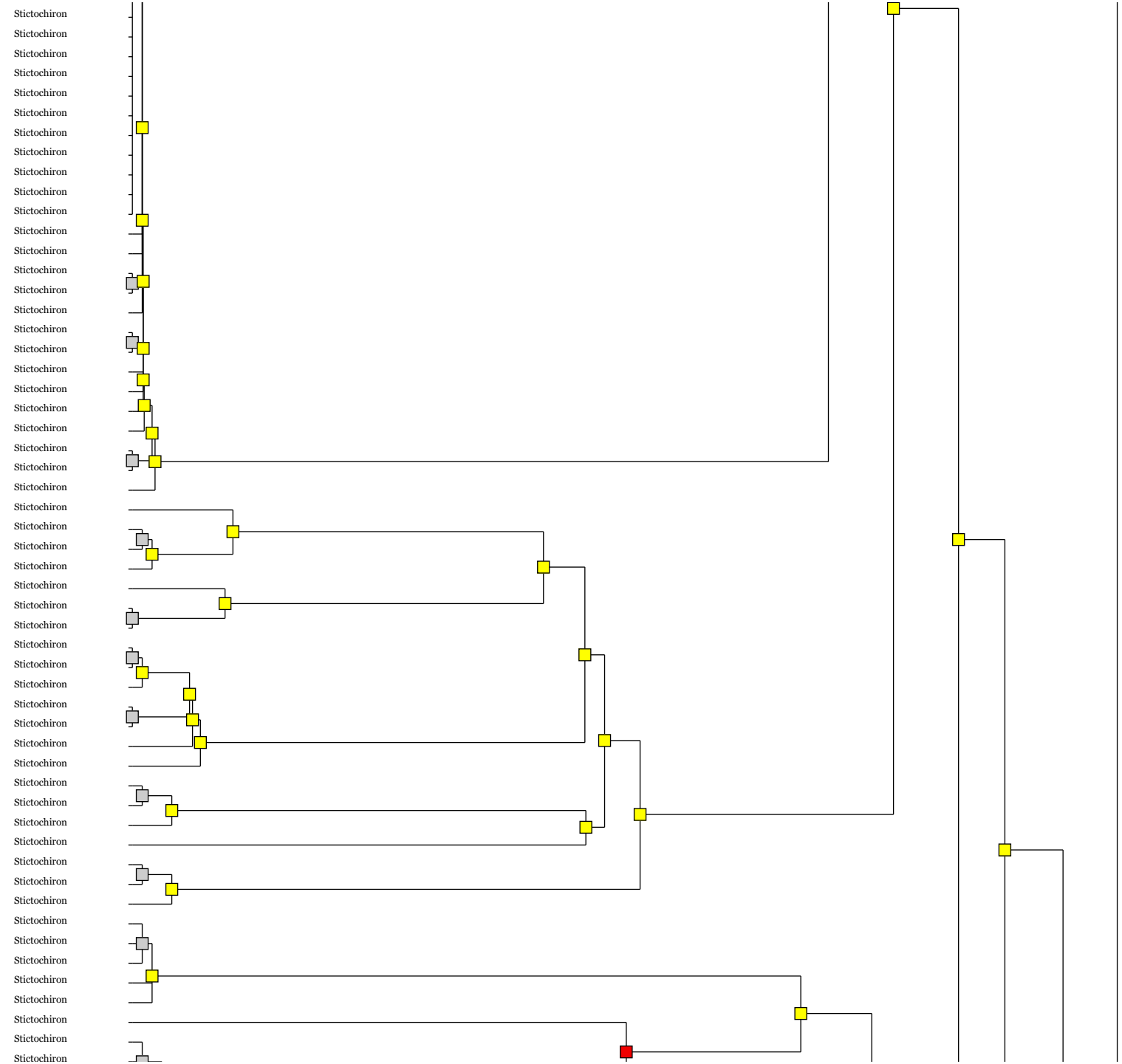
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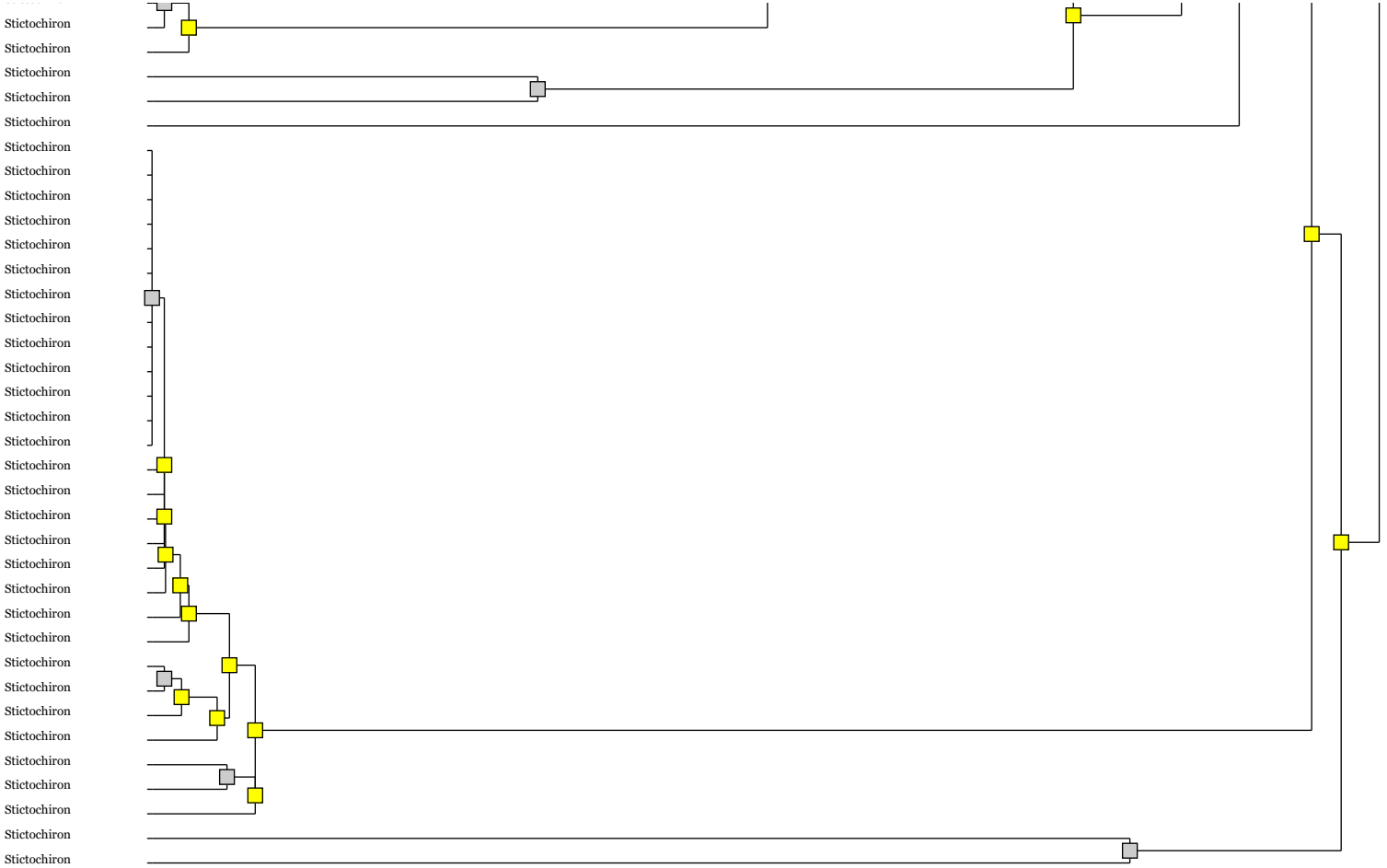
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